



PCT09

RAW SEQUENCE LISTING

DATE: 02/19/2004

PATENT APPLICATION: US/09/807,660C

TIME: 11:19:21

Input Set : A:\23495rV3.txt

Output Set: N:\CRF4\02182004\I807660C.raw

3 <110> APPLICANT: Maliszewski, Charles R.
4 Gayle III, Richard B.
5 Marcus, Aaron J.
6 Immunex Corporation
7 Cornell Research Foundation, Inc.
9 <120> TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and
10 Recruitment
12 <130> FILE REFERENCE: 23,495 USA
14 <140> CURRENT APPLICATION NUMBER: US 09/807,660C
15 <141> CURRENT FILING DATE: 2001-09-06
17 <150> PRIOR APPLICATION NUMBER: US 60/104,585
18 <151> PRIOR FILING DATE: 1998-10-16
20 <150> PRIOR APPLICATION NUMBER: US 60/107,466
21 <151> PRIOR FILING DATE: 1998-11-06
23 <150> PRIOR APPLICATION NUMBER: US 60/149,010
24 <151> PRIOR FILING DATE: 1999-08-13
26 <160> NUMBER OF SEQ ID NOS: 37
28 <170> SOFTWARE: PatentIn version 3.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 1599
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (67)..(1596)
39 <400> SEQUENCE: 1
40 ccacaccaag cagcggtctgg ggggggggaaa gacgaggaaa gaggaggaaa acaaaagctg 60
42 ctactt atg gaa gat aca aag gag tct aac gtg aag aca ttt tgc tcc 108
43 Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser
44 1 5 10
46 aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156
47 Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
48 15 20 25 30
50 gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204
51 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
52 35 40 45
54 gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252
55 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
56 50 55 60
58 tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 300
59 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
60 65 70 75
62 cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 348

P.6
ENTERED

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63 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
64      80                      85                      90
66 gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 396
67 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
68 95                      100                      105                      110
70 aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt 444
71 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
72                      115                      120                      125
74 tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa 492
75 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu
76                      130                      135                      140
78 gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac 540
79 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
80                      145                      150                      155
82 tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa 588
83 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
84                      160                      165                      170
86 ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt 636
87 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
88 175                      180                      185                      190
90 cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag 684
91 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln
92                      195                      200                      205
94 gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act 732
95 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
96                      210                      215                      220
98 ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa 780
99 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
100                      225                      230                      235
102 ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg 828
103 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
104                      240                      245                      250
106 tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att 876
107 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
108 255                      260                      265                      270
110 cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga 924
111 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
112                      275                      280                      285
114 tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc 972
115 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
116                      290                      295                      300
118 aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt 1020
119 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
120                      305                      310                      315
122 att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac 1068
123 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
124                      320                      325                      330
126 acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 1116
127 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu

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128 335          340          345          350
130 cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg 1164
131 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
132          355          360          365
134 atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1212
135 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
136          370          375          380
138 act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1260
139 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
140          385          390          395
142 aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1308
143 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
144          400          405          410
146 tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1356
147 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
148 415          420          425          430
150 gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1404
151 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
152          435          440          445
154 gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1452
155 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
156          450          455          460
158 cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc 1500
159 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val
160          465          470          475
162 ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata 1548
163 Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile
164          480          485          490
166 ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta 1596
167 Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
168 495          500          505          510
170 tag 1599
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 510
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 2
179 Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn
180 1 5 10 15
182 Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
183 20 25 30
185 Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
186 35 40 45
188 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
189 50 55 60
191 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
192 65 70 75 80
194 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
195 85 90 95

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197 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
198          100          105          110
200 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
201          115          120          125
203 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
204          130          135          140
206 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
207 145          150          155          160
209 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
210          165          170          175
212 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
213          180          185          190
215 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
216          195          200          205
218 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
219          210          215          220
221 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
222 225          230          235          240
224 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
225          245          250          255
227 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
228          260          265          270
230 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
231          275          280          285
233 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
234          290          295          300
236 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
237 305          310          315          320
239 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
240          325          330          335
242 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
243          340          345          350
245 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
246          355          360          365
248 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
249          370          375          380
251 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
252 385          390          395          400
254 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
255          405          410          415
257 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
258          420          425          430
260 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
261          435          440          445
263 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
264          450          455          460
266 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
267 465          470          475          480
269 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu

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270                               485                               490                               495
272 Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
273                               500                               505                               510
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277 <211> LENGTH: 476
278 <212> TYPE: PRT
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion
283      construct of human CD39
285 <400> SEQUENCE: 3
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287   1           5           10           15
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290           20           25           30
292 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
293   35           40           45
295 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
296   50           55           60
298 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
299   65           70           75           80
301 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
302           85           90           95
304 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
305           100          105          110
307 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
308           115          120          125
310 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
311           130          135          140
313 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
314 145           150          155          160
316 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
317           165          170          175
319 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
320           180          185          190
322 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
323           195          200          205
325 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
326           210          215          220
328 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
329 225           230          235          240
331 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
332           245          250          255
334 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
335           260          265          270
337 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
338           275          280          285
340 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
341           290          295          300

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 39

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:32,33,34,35,36,37

VERIFICATION SUMMARY

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L:398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:32